Claims

1. Method for increasing abiotic stress tolerance of plants, comprising the steps of introducing a genetic modification in said plants and selecting for modulated expression in said plants of a nucleic acid sequence encoding a protein chosen from the group of
   (i) proteins belonging to the family of CHMP proteins;
   (ii) proteins comprising a SEC14 domain and exhibiting lipid transfer activity;
   (iii) CRYO5 like plant proteins comprising a RING finger domain, a serine rich domain and an acid domain which comprises the signature "HDQHRDMRLDIDNMSYEELLALEERIG", in which no more than 6 substitutions may occur.

2. A method for increasing abiotic stress tolerance of plants or yeast, comprising the steps of introducing a genetic modification in said plant or yeast and selecting for modulated expression in said plant or yeast of a nucleic acid encoding a protein, and/or modulated activity in a plant or yeast of a protein, which protein
   (a) comprises the sequence as given in SEQ ID NO 2, 4, 6, 8 or 10;
   (b) comprises a sequence having at least 50 %, alternatively 60%, 70%, 80%, preferably 90%, more preferably 95%, 96%, 97%, 98% or 99% sequence identity to the full length sequence as given in SEQ ID NO 2, 4, 6, 8 or 10;
   (c) comprises a substitution variant or insertion variant of (a);
   (d) according to any of (a) to (c), comprises substitutions with corresponding naturally or non-naturally altered amino acids;
   (e) comprises a functional fragment of any of (a) to (d).

3. Method of claim 1 or 2, wherein said genetic modification comprises introducing into a plant or yeast an isolated nucleic acid encoding said protein or a functional fragment thereof.

4. Method of any of claims 1 to 3, wherein said abiotic stress is at least one of temperature stress, osmotic stress, drought stress, salt stress or oxidative stress, preferably said abiotic stress is cold stress.

5. A method for producing a transgenic plant having increased tolerance to abiotic stress relative to corresponding wild type plants, which method comprises the steps of:
   (i) introducing into a plant cell a nucleic acid encoding a protein as listed in claim 1 or 2 or a functional fragment thereof; and
   (ii) regenerating and/or growing a mature plant from said plant cell.

6. A plant, plant part or plant cell obtained by the method according to any of claims 1 to 5.

7. Plants with increased tolerance to abiotic stress, preferably cold stress, which plants have increased expression of a nucleic acid encoding a protein, or a functional fragment thereof, chosen from the group of
   (i) proteins belonging to the family of CHMP proteins;
   (ii) proteins comprising a SEC14 domain and exhibiting lipid transfer activity;
   (iii) CRYO5 like plant proteins comprising a RING finger domain, a serine rich domain and an acid domain which comprises the signature "HDQHRDMRLDIDNMSYEELLALEERIG", in which no more than 6 substitutions may occur;
   when compared to corresponding wild type plants.

8. Plants with increased tolerance to abiotic stress, preferably cold stress, which plants have increased expression of a nucleic acid encoding a protein as listed in claim 2, when compared to corresponding wild type plants.

9. A harvestable part, organ, tissue, propagation material, seed, and ancestors or progeny of a plant according to any of claims 6 to 8.

10. A method for producing a transgenic yeast cell having increased tolerance to abiotic stress relative to corresponding wild type yeast cells, which method comprises introducing into a yeast cell a nucleic acid encoding a protein as listed in claim 1 or 2, or a functional fragment thereof.

11. A transgenic yeast cell obtained by the method of claim 10.

12. Transgenic yeast cell with increased tolerance to abiotic stress, preferably cold stress, which yeast cell has increased expression of a nucleic acid encoding a protein as listed in claim 1 or 2, or a functional fragment thereof, when compared to corresponding wild type yeast cells.

13. The use of a nucleic acid encoding a protein as listed in claim 2 for modifying abiotic stress tolerance in yeast, a plant, plant part or plant cell, wherein said abiotic stress is at least one of temperature stress, osmotic stress, drought stress, salt stress or

oxidative stress, preferably said abiotic stress is temperature stress, more preferably said abiotic stress is cold stress.

14. The use of a nucleic acid encoding a protein, or a functional fragment thereof, chosen from the group of

(i) proteins belonging to the family of CHMP proteins;

(ii) proteins comprising a SEC14 domain and exhibiting lipid transfer activity;

(iii) CRYO5 like plant proteins comprising a RING finger domain, a serine rich domain and an acid domain which comprises the signature "HDQHRDMRLDIDNMSYEELLALEERIG", in which no more than 6 substitutions may occur;

for modifying abiotic stress tolerance in yeast, a plant, plant part or plant cell, wherein said abiotic stress is at least one of temperature stress, osmotic stress, drought stress, salt stress or oxidative stress, preferably said abiotic stress is temperature stress, more preferably said abiotic stress is cold stress.

15. The use of a protein according to claim 2 for modifying abiotic stress tolerance in yeast, a plant, plant part or plant cell, wherein said abiotic stress is at least one of temperature stress, osmotic stress, drought stress salt stress or oxidative stress, preferably said abiotic stress is temperature stress, more preferably said abiotic stress is cold stress.

16. The use of a protein, or a functional fragment thereof, chosen from the group of

(i) proteins belonging to the family of CHMP proteins;

(ii) proteins comprising a SEC14 domain and exhibiting lipid transfer activity;

(iii) CRYO5 like plant proteins comprising a RING finger domain, a serine rich domain and an acid domain which comprises the signature "HDQHRDMRLDIDNMSYEELLALEERIG", in which no more than 6 substitutions may occur;

for modifying abiotic stress tolerance in yeast, a plant, plant part or plant cell, wherein said abiotic stress is at least one of temperature stress, osmotic stress, drought stress salt stress or oxidative stress, preferably said abiotic stress is temperature stress, more preferably said abiotic stress is cold stress.

17. The use of a nucleic acid encoding a protein as listed in claim 1 or 2, or the use of a protein as listed in claim 1 or 2 as a selectable marker in plants or other organisms.

18. An isolated protein

(a) comprising the sequence as given in SEQ ID NO 2, 4, 6, 8 or 10;

(b) comprising a sequence having at least

i. 76 %, alternatively 80%, preferably 90%, more preferably 95%, 96%, 97%, 98% or 99% sequence identity to the full length sequence as given in SEQ ID NO 2;

ii. 55 %, alternatively 60%, 70%, 80%, preferably 90%, more preferably 95%, 96%, 97%, 98% or 99% sequence identity to the full length sequence as given in SEQ ID NO 4;

iii. 90.5 %, alternatively 90.6%, 90.7%, 90.8%, 90.9%, preferably 91%, 92%, 93%, 94% more preferably 95%, 96%, 97%, 98% or 99% sequence identity to the full length sequence as given in SEQ ID NO 6;

iv. 50 %, alternatively 60%, 70%, 80%, preferably 90%, more preferably 95%, 96%, 97%, 98% or 99% sequence identity to the full length sequence as given in SEQ ID NO 8;

v. 50 %, alternatively 60%, 70%, 80%, preferably 90%, more preferably 95%, 96%, 97%, 98% or 99% sequence identity to the full length sequence as given in SEQ ID NO 10;

(c) comprising a substitution variant or insertion variant of (a);

(d) according to any of (a) to (c), comprising substitutions with corresponding naturally or non-naturally altered amino acids.

19. An isolated nucleic acid encoding a protein according to claim 19, the complement thereof or a part thereof.

20. A genetic construct comprising:

(i) an isolated nucleic acid encoding a plant protein

(a) comprising the sequence as given in SEQ ID NO 2, 4, 6, 8 or 10;

(b) comprising a sequence having at least 50 %, alternatively 60%, 70%, 80%, preferably 90%, more preferably 95%, 96%, 97%, 98% or 99% sequence identity to the full length sequence as given in SEQ ID NO 2, 4, 6, 8 or 10;

(c) comprising a substitution variant or insertion variant of (a);

(d) according to any of (a) to (c), comprising substitutions with corresponding naturally or non-naturally altered amino acids;

(ii) a regulatory element operably linked to the nucleic acid of (i), which regulatory element is a plant and/or yeast expressible promoter; and optionally

(iii) a transcription termination sequence.

21. A host cell comprising an isolated nucleic acid encoding a protein according to claim 18, wherein said host cell is a bacterial, yeast, fungal, plant or animal cell.

22. Screening method for identifying nucleic acids capable of modifying tolerance or resistance to cold stress conditions in plants or yeast, said method comprising the steps of:
(i) providing a cDNA library of coding sequences from an organism;
(ii) introducing these coding sequences in an expressible format into wild type yeast cells;
(iii) growing the yeast cells of (ii) under conditions of cold stress;
(iv) identifying differences between the transgenic yeast cells and wild type yeast cells, preferably identifying differences in growth rate;
(v) isolating nucleic acids from the transgenic yeast cells that differ from the wild type yeast cells.

23. Method according to claim 22, wherein said wild type yeast cells are wild type *Saccharomyces cerevisiae* yeast cells, preferably wild type *Saccharomyces cerevisiae* W303 yeast cells.

24. Method according to claim 22, wherein said organism is a plant, preferably a salt treated plant, more preferably a salt treated halophytic plant or a part thereof, most preferably salt treated *Beta vulgaris* or a part thereof.

25. Use of the screening method according to any of claims 22 to 24 for identifying nucleic acids encoding proteins capable of conferring cold stress tolerance to plant cells or yeast cells.

26. Method for increasing cold tolerance of yeast cells, comprising downregulating expression in yeast of a nucleic acid encoding a glycerol phosphate dehydrogenase and/or inhibiting activity of a glycerol phosphate dehydrogenase.